GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:58:44 ; Search time 48 Seconds
(without alignments)
193.105 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match %	Length	DB	ID	Description
	1	15	71.4	22	4	US-09-235-742-19	Sequence 19, Appl
	2	15	71.4	22	4	US-09-347-343-32	Sequence 32, Appl
	3	15	71.4	22	4	US-09-820-484-1	Sequence 1, Appli
	4	15	71.4	22	4	US-09-820-484-3	Sequence 3, Appli
	5	15	71.4	22	4	US-09-774-403A-1	Sequence 1, Appli
	6	14	66.7	816	3	US-08-776-251-10	Sequence 10, Appl
c	7	14	66.7	816	3	US-08-776-251-10	Sequence 10, Appl
c	8	14	66.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	9	14	66.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	10	13	61.9	321	3	US-09-060-756-260	Sequence 260, App
c	11	13	61.9	321	3	US-09-240-274-197	Sequence 197, App
	12	13	61.9	321	4	US-09-670-314-260	Sequence 260, App
	13	13	61.9	462	4	US-09-252-991A-16046	Sequence 16046, A
c	14	13	61.9	573	4	US-09-252-991A-9162	Sequence 9162, Ap
c	15	13	61.9	663	4	US-09-252-991A-9246	Sequence 9246, Ap
c	16	13	61.9	762	4	US-09-252-991A-16554	Sequence 16554, A
	17	13	61.9	813	4	US-09-107-532A-1566	Sequence 1566, Ap
	18	13	61.9	1221	4	US-09-252-991A-8921	Sequence 8921, Ap
c	19	13	61.9	1461	4	US-09-252-991A-9074	Sequence 9074, Ap
	20	13	61.9	1545	4	US-09-252-991A-8710	Sequence 8710, Ap
c	21	13	61.9	1986	4	US-09-252-991A-16328	Sequence 16328, A
	22	13	61.9	2091	4	US-09-252-991A-15954	Sequence 15954, A
	23	13	61.9	43804	4	US-09-171-461-1	Sequence 1, Appli
c	24	12	57.1	20	3	US-09-286-098-11	Sequence 11, Appl
c	25	12	57.1	20	4	US-09-325-193A-91	Sequence 91, Appl
	26	12	57.1	22	2	US-08-882-704A-18	Sequence 18, Appl
c	27	12	57.1	22	2	US-08-882-704A-18	Sequence 18, Appl
	28	12	57.1	22	4	US-09-151-957-18	Sequence 18, Appl
c	29	12	57.1	22	4	US-09-151-957-18	Sequence 18, Appl
c	30	12	57.1	71	3	US-08-633-768A-12	Sequence 12, Appl
c	31	12	57.1	77	1	US-08-399-412A-58	Sequence 58, Appl
c	32	12	57.1	160	3	US-08-633-768A-14	Sequence 14, Appl
c	33	12	57.1	186	4	US-09-328-352-3855	Sequence 3855, Ap
	34	12	57.1	212	4	US-09-313-294A-2448	Sequence 2448, Ap
	35	12	57.1	268	4	US-09-313-294A-2857	Sequence 2857, Ap
c	36	12	57.1	283	4	US-09-313-294A-4896	Sequence 4896, Ap
	37	12	57.1	288	4	US-09-252-991A-69	Sequence 69, Appl
c	38	12	57.1	378	4	US-09-252-991A-5259	Sequence 5259, Ap
	39	12	57.1	406	3	US-09-060-756-563	Sequence 563, App
	40	12	57.1	406	4	US-09-670-314-563	Sequence 563, App
	41	12	57.1	432	4	US-09-252-991A-3530	Sequence 3530, Ap
	42	12	57.1	441	4	US-09-252-991A-4565	Sequence 4565, Ap
c	43	12	57.1	658	3	US-08-861-774E-69	Sequence 69, Appl
	44	12	57.1	806	4	US-09-198-119C-78	Sequence 78, Appl
c	45	12	57.1	813	4	US-09-107-532A-1566	Sequence 1566, Ap

ALIGNMENTS

RESULT 1
US-09-235-742-19
; Sequence 19, Application US/09235742
; Patent No. 6498148
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Immunization-Free Methods for Treating
; TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and
; TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1
; TITLE OF INVENTION: Phenotype
; FILE REFERENCE: 6510-170CON4
; CURRENT APPLICATION NUMBER: US/09/235,742
; CURRENT FILING DATE: 1999-01-21
; EARLIER APPLICATION NUMBER: 08/927,120
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 08/593,554
; EARLIER FILING DATE: 1996-01-30
; EARLIER APPLICATION NUMBER: 08/725,968
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: 60/028,118
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant or Synthetic Sequence
US-09-235-742-19

Query Match 71.4%; Score 15; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTCGAGATGA 20
||||||||||||||||
Db 8 GAACGTTCGAGATGA 22

RESULT 2
US-09-347-343-32
; Sequence 32, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A

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;  CURRENT FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: synthetic oligonucleotide
US-09-347-343-32

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 3
US-09-820-484-1
; Sequence 1, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: disulfide thymine
US-09-820-484-1

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 4
US-09-820-484-3
; Sequence 3, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorothioate ISS-ODN
US-09-820-484-3

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 5
US-09-774-403A-1
; Sequence 1, Application US/09774403A
; Patent No. 6552006
; GENERAL INFORMATION:
;  APPLICANT: Eyal Raz
;  APPLICANT:  Richard Kornbluth
;  APPLICANT:  Antonio Catanzaro
;  APPLICANT:  Tomoko Hayashi
;  APPLICANT:  Dennis Carson
;  TITLE OF INVENTION: Immunomodulatory Polynucleotides in
;  TITLE OF INVENTION:  Treatment of Infection by an Intracellular Pathogen
;  FILE REFERENCE: UCAL166
;  CURRENT APPLICATION NUMBER: US/09/774,403A
;  CURRENT FILING DATE:  2002-04-15
;  PRIOR APPLICATION NUMBER: 60/179,353
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Immunomodulatory sequence
US-09-774-403A-1

  Query Match             71.4%;  Score 15;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 6
US-08-776-251-10
; Sequence 10, Application US/08776251
; Patent No. 6025340
;  GENERAL INFORMATION:
;    APPLICANT:  Springer, Caroline J
;    APPLICANT:  Marais, Richard
;    TITLE OF INVENTION:  Surface expression of enzyme in gene directed prodrug therapy
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon & Vanderhye
```

```
;      STREET:  1100 No. 6025340th Glebe Road, 8th Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  USA
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/776,251.
;      FILING DATE:  31-JAN-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01782
;      FILING DATE:  27-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9415167.7
;      FILING DATE:  27-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arthur R. Crawford
;      REGISTRATION NUMBER:  25,327
;      REFERENCE/DOCKET NUMBER:  620-20
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  816 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-776-251-10

  Query Match             66.7%;  Score 14;  DB 3;  Length 816;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGA 17
              ||||||||||||||
Db        619 TCGAACGTTCGAGA 632


RESULT 7
US-08-776-251-10/c
; Sequence 10, Application US/08776251
; Patent No. 6025340
;  GENERAL INFORMATION:
;    APPLICANT:  Springer, Caroline J
;    APPLICANT:  Marais, Richard
;    TITLE OF INVENTION:  Surface expression of enzyme in gene directed prodrug therapy
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon & Vanderhye
;      STREET:  1100 No. 6025340th Glebe Road, 8th Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  USA
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/776,251
;      FILING DATE:  31-JAN-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01782
;      FILING DATE:  27-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9415167.7
;      FILING DATE:  27-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arthur R. Crawford
;      REGISTRATION NUMBER:  25,327
;      REFERENCE/DOCKET NUMBER:  620-20
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  816 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-776-251-10

  Query Match             66.7%;  Score 14;  DB 3;  Length 816;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGA 17
              ||||||||||||||
Db        801 TCGAACGTTCGAGA 788


RESULT 8
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             66.7%;  Score 14;  DB 3;  Length 4403765;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCG 14
              ||||||||||||||
Db     735047 TCGTCGAACGTTCG 735034


RESULT 9
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
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;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             66.7%;  Score 14;  DB 3;  Length 4411529;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCG 14
              ||||||||||||||
Db     733615 TCGTCGAACGTTCG 733602


RESULT 10
US-09-060-756-260
; Sequence 260, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
;  APPLICANT: Cole, Stewart
;  APPLICANT: Buchrieser-Brosch, Roland
;  APPLICANT: Gordon, Stephen
;  APPLICANT: Billault, Alain
;  TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
;  TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
;  TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
;  FILE REFERENCE: 3495-0169
;  CURRENT APPLICATION NUMBER: US/09/060,756
;  CURRENT FILING DATE: 1998-04-16
;  NUMBER OF SEQ ID NOS: 743
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 260
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (various positions within the sequence)
;   OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-260

  Query Match             61.9%;  Score 13;  DB 3;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ACGTTCGAGATGA 20
              |||||||||||||
Db         75 ACGTTCGAGATGA 87


RESULT 11
US-09-240-274-197/c
; Sequence 197, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 197
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH8
US-09-240-274-197

  Query Match             61.9%;  Score 13;  DB 3;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CGAACGTTCGAGA 17
              |||||||||||||
Db        292 CGAACGTTCGAGA 280


RESULT 12
US-09-670-314-260
; Sequence 260, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
;  APPLICANT: Cole, Stewart
;  APPLICANT:  Buchrieser-Brosch, Roland
;  APPLICANT:  Gordon, Stephen
;  APPLICANT:  Billault, Alain
;  TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
;  TITLE OF INVENTION:  THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
;  TITLE OF INVENTION:  LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
;  FILE REFERENCE: 3495-0169
;  CURRENT APPLICATION NUMBER: US/09/670,314
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER: 09/060,756
;  PRIOR FILING DATE: 1998-04-16
;  NUMBER OF SEQ ID NOS: 743
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 260
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (various positions within the sequence)
;   OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-670-314-260

  Query Match             61.9%;  Score 13;  DB 4;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ACGTTCGAGATGA 20
              |||||||||||||
Db         75 ACGTTCGAGATGA 87


RESULT 13
US-09-252-991A-16046
; Sequence 16046, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 16046
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16046

  Query Match             61.9%;  Score 13;  DB 4;  Length 462;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          8 ACGTTCGAGATGA 20
              |||||||||||||
Db         34 ACGTTCGAGATGA 46


RESULT 14
US-09-252-991A-9162/c
; Sequence 9162, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 9162
;   LENGTH: 573
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (17)
;   OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-9162

  Query Match             61.9%;  Score 13;  DB 4;  Length 573;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGAT 18
              |||||||||||||
Db        286 GAACGTTCGAGAT 274


RESULT 15
US-09-252-991A-9246/c
; Sequence 9246, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 9246
;   LENGTH: 663
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9246

  Query Match             61.9%;  Score 13;  DB 4;  Length 663;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGAT 18
              |||||||||||||
Db         45 GAACGTTCGAGAT 33


Search completed: December 19, 2003, 13:47:04
Job time : 61 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:58:44 ; Search time 149 Seconds
(without alignments)
469.639 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2211978 seqs, 1666101734 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	21	15	US-10-033-243-132	Sequence 132, App
2	19	90.5	19	11	US-09-927-422A-16	Sequence 16, Appl
3	19	90.5	19	13	US-10-176-883-41	Sequence 41, Appl
4	19	90.5	19	13	US-10-177-826-41	Sequence 41, Appl
5	19	90.5	19	15	US-10-033-243-19	Sequence 19, Appl
6	19	90.5	22	13	US-10-176-883-52	Sequence 52, Appl
7	19	90.5	22	13	US-10-177-826-52	Sequence 52, Appl
8	19	90.5	22	15	US-10-033-243-30	Sequence 30, Appl
9	16	76.2	18	13	US-10-176-883-36	Sequence 36, Appl
10	16	76.2	18	13	US-10-177-826-36	Sequence 36, Appl
11	16	76.2	18	15	US-10-033-243-14	Sequence 14, Appl
12	16	76.2	66	13	US-10-176-883-139	Sequence 139, App
13	16	76.2	66	13	US-10-177-826-139	Sequence 139, App
14	15	71.4	20	13	US-09-848-986-21	Sequence 21, Appl
15	15	71.4	20	15	US-10-233-121A-21	Sequence 21, Appl
16	15	71.4	22	9	US-09-802-686-1	Sequence 1, Appli
17	15	71.4	22	9	US-09-802-686-2	Sequence 2, Appli
18	15	71.4	22	9	US-09-802-685-1	Sequence 1, Appli
19	15	71.4	22	9	US-09-802-685-2	Sequence 2, Appli
20	15	71.4	22	9	US-09-791-500-1	Sequence 1, Appli
21	15	71.4	22	9	US-09-802-376-1	Sequence 1, Appli
22	15	71.4	22	9	US-09-802-376-2	Sequence 2, Appli
23	15	71.4	22	9	US-09-802-370-1	Sequence 1, Appli
24	15	71.4	22	9	US-09-802-370-2	Sequence 2, Appli
25	15	71.4	22	10	US-09-802-445-1	Sequence 1, Appli
26	15	71.4	22	10	US-09-802-445-2	Sequence 2, Appli
27	15	71.4	22	10	US-09-820-484-1	Sequence 1, Appli
28	15	71.4	22	10	US-09-820-484-3	Sequence 3, Appli
29	15	71.4	22	10	US-09-828-505-1	Sequence 1, Appli
30	15	71.4	22	10	US-09-967-881-2	Sequence 2, Appli
31	15	71.4	22	11	US-09-927-422A-1	Sequence 1, Appli
32	15	71.4	22	11	US-09-927-422A-2	Sequence 2, Appli
33	15	71.4	22	11	US-09-738-046A-3	Sequence 3, Appli
34	15	71.4	22	11	US-09-927-884-1	Sequence 1, Appli
35	15	71.4	22	11	US-09-927-884-2	Sequence 2, Appli
36	15	71.4	22	13	US-09-802-359-1	Sequence 1, Appli
37	15	71.4	22	13	US-09-802-359-2	Sequence 2, Appli
38	15	71.4	22	13	US-09-967-464-19	Sequence 19, Appl
39	15	71.4	22	13	US-10-214-799-2	Sequence 2, Appli
40	15	71.4	22	13	US-10-340-275-1	Sequence 1, Appli
41	15	71.4	22	13	US-10-340-275-3	Sequence 3, Appli
42	15	71.4	22	13	US-10-339-885-1	Sequence 1, Appli
43	15	71.4	22	13	US-10-339-885-3	Sequence 3, Appli
44	15	71.4	22	13	US-09-848-986-1	Sequence 1, Appli
45	15	71.4	22	13	US-10-176-883-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-033-243-132
; Sequence 132, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 377882001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-132

Query Match 100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TCGTCGAACGTTCGAGATGAT 21
              |||||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATGAT 21
```

RESULT 2
US-09-927-422A-16
; Sequence 16, Application US/09927422A
; Publication No. US20030022852A1
; GENERAL INFORMATION:

```
;  APPLICANT: Van Nest, Gary
;  APPLICANT:  Tuck, Stephen
;  APPLICANT:  Fearon, Karen L.
;  APPLICANT:  Dina, Dino
;  TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
;  TITLE OF INVENTION:  FORMULATIONS AND METHODS FOR USE THEREOF
;  FILE REFERENCE: 377882001420
;  CURRENT APPLICATION NUMBER: US/09/927,422A
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/802,359
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: U.S. 60/188,30
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-927-422A-16

  Query Match           90.5%;  Score 19;  DB 11;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 0.065;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 3
US-10-176-883-41
; Sequence 41, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-41

  Query Match           90.5%;  Score 19;  DB 13;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 0.065;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 4
US-10-177-826-41
; Sequence 41, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-177-826-41

  Query Match           90.5%;  Score 19;  DB 13;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 0.065;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 5
US-10-033-243-19
; Sequence 19, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-19

  Query Match           90.5%;  Score 19;  DB 15;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 0.065;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 6
US-10-176-883-52
; Sequence 52, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
```

; TITLE OF INVENTION: METHODS OF USING THE SAME-I
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-176-883-52

Query Match 90.5%; Score 19; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||||
Db 4 TCGTCGAACGTTCGAGATG 22

RESULT 7
US-10-177-826-52
; Sequence 52, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-II
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-52

Query Match 90.5%; Score 19; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||||
Db 4 TCGTCGAACGTTCGAGATG 22

RESULT 8
US-10-033-243-30
; Sequence 30, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 377882001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-30

Query Match 90.5%; Score 19; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
||||||||||||||||||||
Db 4 TCGTCGAACGTTCGAGATG 22

RESULT 9
US-10-176-883-36
; Sequence 36, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-I
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-176-883-36

Query Match 76.2%; Score 16; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTTCGAGATG 19
||||||||||||||||
Db 3 TCGAACGTTCGAGATG 18

RESULT 10
US-10-177-826-36
; Sequence 36, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-II
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883

```
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-177-826-36

  Query Match             76.2%;  Score 16;  DB 13;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATG 19
              ||||||||||||||||
Db          3 TCGAACGTTCGAGATG 18


RESULT 11
US-10-033-243-14
; Sequence 14, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
;  APPLICANT: FEARON, Karen L.
;  APPLICANT:  DINA, Dino
;  TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME
;  FILE REFERENCE: 377882001800
;  CURRENT APPLICATION NUMBER: US/10/033,243
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/258,675
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-14

  Query Match             76.2%;  Score 16;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATG 19
              ||||||||||||||||
Db          3 TCGAACGTTCGAGATG 18


RESULT 12
US-10-176-883-139
; Sequence 139, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-I
;  FILE REFERENCE: 377882002000
;  CURRENT APPLICATION NUMBER: US/10/176,883
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
;   LENGTH: 66
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-176-883-139

  Query Match             76.2%;  Score 16;  DB 13;  Length 66;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGAT 21
              ||||||||||||||||
Db          8 GAACGTTCGAGATGAT 23


RESULT 13
US-10-177-826-139
; Sequence 139, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
;  APPLICANT: Fearon, Karen
;  APPLICANT:  Dina, Dino
;  APPLICANT:  Tuck, Stephen
;  TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
;  TITLE OF INVENTION:  METHODS OF USING THE SAME-II
;  FILE REFERENCE: 377882002001
;  CURRENT APPLICATION NUMBER: US/10/177,826
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/299,883
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/375,253
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
;   LENGTH: 66
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-177-826-139

  Query Match             76.2%;  Score 16;  DB 13;  Length 66;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGAT 21
              ||||||||||||||||
Db          8 GAACGTTCGAGATGAT 23


RESULT 14
US-09-848-986-21
; Sequence 21, Application US/09848986
; Publication No. US20030176373A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Lois, Augusto F.
;  APPLICANT:  Takabayashi, Kenji
;  TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
;  TITLE OF INVENTION:  Methods of Use Thereof
;  FILE REFERENCE: 06510168US1
;  CURRENT APPLICATION NUMBER: US/09/848,986
;  CURRENT FILING DATE:  2001-05-03
;  PRIOR APPLICATION NUMBER: us 60/262321
;  PRIOR FILING DATE: 2001-01-17
;  PRIOR APPLICATION NUMBER: us 60/202,274
;  PRIOR FILING DATE: 2000-05-05
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ISS-ODN
US-09-848-986-21

Query Match 71.4%; Score 15; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTCGAGATGA 20
||||||||||||||
Db 6 GAACGTTCGAGATGA 20

RESULT 15
US-10-233-121A-21
; Sequence 21, Application US/10233121A
; Publication No. US20030125284A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, EYAL
; APPLICANT: LOIS, AUGUSTO
; APPLICANT: TAKABAYASHI, KENJI
; TITLE OF INVENTION: AGENTS THAT MODULATE DNA-PK ACTIVITY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: UCAL-168DIV
; CURRENT APPLICATION NUMBER: US/10/233,121A
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 09/848,986
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/202,274
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/262,321
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphodiester or phosphorothioate oligonucleotide
US-10-233-121A-21

Query Match 71.4%; Score 15; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTCGAGATGA 20
||||||||||||||
Db 6 GAACGTTCGAGATGA 20

Search completed: December 19, 2003, 13:43:23
Job time : 151 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:58:44 ; Search time 1308 Seconds
(without alignments)
390.209 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15	71.4	194	13	BU095678	BU095678 tca-163 t
c	2	15	71.4	337	12	BI511039	BI511039 BB160004A
c	3	15	71.4	390	9	AI945022	AI945022 bs08b02.y
c	4	15	71.4	432	12	BI510669	BI510669 BB160003A
	5	15	71.4	609	28	AQ623639	AQ623639 HS_5377_A
	6	15	71.4	728	28	BH816458	BH816458 AM__Ba002
c	7	15	71.4	842	29	BZ391656	BZ391656 EINCQ64TR
c	8	15	71.4	889	14	CD375545	CD375545 PTMM00709
c	9	15	71.4	913	13	BX455352	BX455352 BX455352
c	10	15	71.4	1220	29	CC235774	CC235774 CH261-139
c	11	14	66.7	108	11	CNS09N54	BX066068 Single re
	12	14	66.7	168	14	R04873	R04873 pk33h10.r1
c	13	14	66.7	298	9	AA186214	AA186214 T3860 MVA
c	14	14	66.7	348	11	CNS09Q90	BX070096 Single re
	15	14	66.7	387	12	BI507844	BI507844 BB170008B
	16	14	66.7	414	12	BI505056	BI505056 BB170012B
	17	14	66.7	424	14	CB333691	CB333691 TgESTzyf6
c	18	14	66.7	433	12	BM629296	BM629296 170006874
	19	14	66.7	439	28	AQ252378	AQ252378 HS_2262_A
c	20	14	66.7	466	14	CA302582	CA302582 taa13b12.
c	21	14	66.7	469	11	CNS09GNZ	BX057675 Single re
	22	14	66.7	484	9	AA097939	AA097939 mn82g01.r
c	23	14	66.7	486	12	BM636144	BM636144 170006875
c	24	14	66.7	492	12	BM652631	BM652631 170006873
c	25	14	66.7	493	12	BM644091	BM644091 170006873
c	26	14	66.7	499	12	BM597612	BM597612 170006874
c	27	14	66.7	504	12	BM611518	BM611518 170006871
	28	14	66.7	512	12	BM866297	BM866297 mgcs005xE
	29	14	66.7	513	14	CB358730	CB358730 ZF001-P00
	30	14	66.7	521	28	BH899325	BH899325 Ots00392
c	31	14	66.7	527	12	BM618536	BM618536 170006874
c	32	14	66.7	528	12	BM618261	BM618261 170006874
c	33	14	66.7	528	12	BM632494	BM632494 170006875
	34	14	66.7	528	29	TA99D10P	AL460276 T. brucei
c	35	14	66.7	533	12	BM641866	BM641866 170006873
	36	14	66.7	534	28	AQ407920	AQ407920 HS_5055_B
c	37	14	66.7	541	9	AL695492	AL695492 AL695492
c	38	14	66.7	544	12	BI511012	BI511012 BB160004A
c	39	14	66.7	546	12	BM649585	BM649585 170006873
c	40	14	66.7	549	12	BM650226	BM650226 170006873
c	41	14	66.7	550	12	BM626834	BM626834 170006874
c	42	14	66.7	554	12	BM633500	BM633500 170006875
c	43	14	66.7	556	28	BH899413	BH899413 Ots00480
	44	14	66.7	558	28	AZ216899	AZ216899 Sheared D
c	45	14	66.7	561	12	BM632387	BM632387 170006875

ALIGNMENTS

RESULT 1
BU095678/c
LOCUS BU095678 194 bp mRNA linear EST 14-MAR-2003
DEFINITION tca-163 tca Trypanosoma carassii cDNA clone 01n14 5', mRNA sequence.
ACCESSION BU095678
VERSION BU095678.1 GI:25123402
KEYWORDS EST.
SOURCE Trypanosoma carassii
ORGANISM Trypanosoma carassii
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 194)
AUTHORS Aguero,F., Campo,V., Cremona,L., Jager,A., Di Noia,J.M., Overath,P., Sanchez,D.O. and Frasch,A.C.
TITLE Gene discovery in the freshwater fish parasite Trypanosoma carassii: identification of trans-sialidase-like and mucin-like genes
JOURNAL Infect. Immun. 70 (12), 7140-7144 (2002)
COMMENT Contact: Sanchez DO
Genomics and Bioinformatics
Instituto de Investigaciones Biotecnologicas
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos Aires, Argentina
Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
Email: dsanchez@iib.unsam.edu.ar

```
          Sequences were basecalled with phred and vector was masked with
          crossmatch (see http://www.phrap.org). Sequences were then trimmed
          from both ends to remove low quality bases and masked vector.
          Plate: 01  row: n  column: 14
          Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .194
                     /organism="Trypanosoma carassii"
                     /mol_type="mRNA"
                     /db_xref="taxon:38249"
                     /clone="01n14"
                     /dev_stage="blood trypomastigote"
                     /lab_host="Goldfish (Carassius auratus)"
                     /clone_lib="tca"
                     /note="Vector: pSport1; Blood trypomastigotes were
                     obtained from goldfish and cultured as described (Overath
                     et al. Parasitol Res (1998) 84:343) before obtaining total
                     RNA using TRIzol. cDNA library construction was made from
                     polyA+ mRNA using a poly-dT oligonucleotide as primer. The
                     cDNAs were cloned in a oriented manner using a commercial
                     kit (SuperScript Plasmid System for cDNA Synthesis and
                     Plasmid Cloning, Life Technologies)."
BASE COUNT       60 a     35 c     40 g     59 t
ORIGIN

  Query Match             71.4%;  Score 15;  DB 13;  Length 194;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGA 15
              ||||||||||||||||
Db        149 TCGTCGAACGTTCGA 135


RESULT 2
BI511039/c
LOCUS       BI511039                337 bp    mRNA    linear   EST 08-APR-2002
DEFINITION  BB160004A20G12.5 Bee Brain Normalized Library, BB16 Apis mellifera
            cDNA clone BB160004A20G12 5', mRNA sequence.
ACCESSION   BI511039
VERSION     BI511039.1  GI:15361413
KEYWORDS    EST.
SOURCE      Apis mellifera (honeybee)
  ORGANISM  Apis mellifera
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
REFERENCE   1  (bases 1 to 337)
  AUTHORS   Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L.,
            Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
  TITLE     Annotated expressed sequence tags and cDNA microarrays for studies
            of brain and behavior in the honey bee
  JOURNAL   Genome Res. 12 (4), 555-566 (2002)
  MEDLINE   21929762
   PUBMED   11932240
COMMENT     Contact: Gene E. Robinson
            Department of Entomology
            University of Illinois
            505 S. Goodwin Ave., Urbana, IL 61801, USA
            Tel: 217 265 0309
            Fax: 217 244 3499
            Email: generobi@life.uiuc.edu
            This research was funded by the University of Illinois Critical
            Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
            Award in Functional Genomics to G.E. Robinson and an NSF
            Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Plate: BB160004A20  row: G  column: 12
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 337.
FEATURES             Location/Qualifiers
     source          1. .337
                     /organism="Apis mellifera"
                     /mol_type="mRNA"
                     /strain="mixed strains of European bees,'predominantly
                     A.m. ligustica"
                     /db_xref="taxon:7460"
                     /clone="BB160004A20G12"
                     /sex="female"
                     /tissue_type="brain"
                     /dev_stage="adult worker honey bee"
                     /lab_host="DH10B"
                     /clone_lib="Bee Brain Normalized Library, BB16"
                     /note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1;
                     Site_2: Not1; The BB16 library was contributed by the
                     Soares laboratory and it was  constructed and normalized
                     as described by Bonaldo, M.F., Lennon, G.  and Soares,
                     M.B. (1996), Genome Research 6(9): 791-806. RNA was
                     prepared from dissected brains of adult worker bees of
                     various ages  and various behavioral groups. "
BASE COUNT      123 a     59 c     64 g     91 t
ORIGIN

  Query Match             71.4%;  Score 15;  DB 12;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGA 15
              ||||||||||||||||
Db        264 TCGTCGAACGTTCGA 250


RESULT 3
AI945022/c
LOCUS       AI945022                390 bp    mRNA    linear   EST 08-JAN-2001
DEFINITION  bs08b02.y1 Drosophila melanogaster adult testis library Drosophila
            melanogaster cDNA clone bs08b02 5', mRNA sequence.
ACCESSION   AI945022
VERSION     AI945022.2  GI:9990370
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 390)
  AUTHORS   Andrews,J., Bouffard,G.G., Cheadle,C., Lu,J., Becker,K.G. and
            Oliver,B.
  TITLE     Gene discovery using computational and microarray analysis of
            transcription in the drosophila melanogaster testis
  JOURNAL   Genome Res. 10 (12), 2030-2043 (2000)
  MEDLINE   20568492
   PUBMED   11116097
COMMENT     On Aug 17, 1999 this sequence version replaced gi:5735420.
            Contact: Brian Oliver
            Laboratory of Cellular and Developmental Biology
            NIDDK, National Institutes of Health
            6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
            Fax: (301) 496 5239
            Email: oliver@helix.nih.gov,
            http://www.niddk.nih.gov/intram/people/boliver.htm
            Tissue isolation and library construction performed at the National
            Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
            http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
            and analyses performed by National Institutes of Health Intramural
            Sequencing Center (NISC; see http://www.nisc.nih.gov).
            Plate: 08  row: b  column: 02
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .390
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /strain="y[*] w[67c1]/Y"
                     /db_xref="taxon:7227"
```

/clone="bs08b02"
/sex="male"
/dev_stage="1-5 day adult"
/lab_host="SOLR (Stratagene)"
/clone_lib="Drosophila melanogaster adult testis library"
/note="Organ: testis; Vector: pBlueScript SK (Stratagene); Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5 day adult y[*] w[67c1]/Y males raised at 25oC. RNA isolated using Trizol (Life Technologies) and a single round of Poly(A)+ selection using Oligotex (Qiagen). cDNA library constructed using Stratagene ZAP-cDNA syntesis kit. Oligo dT-primed, size fractionated ~1-6 kb, and directionally cloned at EcoRI and XhoI in Uni-ZAP XR. Following a single round of amplification pBlueScript SK phagemids were mass excised. A distribution channel for clones is being sought, but not currently available. Requests for clones cannot be honored."

BASE COUNT 121 a 77 c 109 g 83 t
ORIGIN

Query Match 71.4%; Score 15; DB 9; Length 390;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGA 15
|||||||||||||||
Db 94 TCGTCGAACGTTCGA 80

RESULT 4
BI510669/c
LOCUS BI510669 432 bp mRNA linear EST 08-APR-2002
DEFINITION BB160003A20G01.5 Bee Brain Normalized Library, BB16 Apis mellifera cDNA clone BB160003A20G01 5', mRNA sequence.
ACCESSION BI510669
VERSION BI510669.1 GI:15361043
KEYWORDS EST.
SOURCE Apis mellifera (honeybee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
REFERENCE 1 (bases 1 to 432)
AUTHORS Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L., Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
TITLE Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee
JOURNAL Genome Res. 12 (4), 555-566 (2002)
MEDLINE 21929762
PUBMED 11932240
COMMENT Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: generobi@life.uiuc.edu
This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
PCR PRimers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
Plate: BB160003A20 row: G column: 01
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 432.
FEATURES Location/Qualifiers
source 1. .432
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="mixed strains of European bees, predominantly A.m. ligustica"
/db_xref="taxon:7460"
/clone="BB160003A20G01"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/clone_lib="Bee Brain Normalized Library, BB16"
/note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1; Site_2: Not1; The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "
BASE COUNT 163 a 69 c 102 g 98 t
ORIGIN

Query Match 71.4%; Score 15; DB 12; Length 432;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGA 15
|||||||||||||||
Db 58 TCGTCGAACGTTCGA 44

RESULT 5
AQ623639
LOCUS AQ623639 609 bp DNA linear GSS 16-JUN-1999
DEFINITION HS_5377_A2_F05_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=953 Col=10 Row=K, genomic survey sequence.
ACCESSION AQ623639
VERSION AQ623639.1 GI:5086119
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 609)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 953 row: K column: 10
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 609.
FEATURES Location/Qualifiers
source 1. .609
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=953 Col=10 Row=K"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
BASE COUNT 185 a 124 c 162 g 125 t 13 others
ORIGIN

Query Match 71.4%; Score 15; DB 28; Length 609;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGA 15
||||||||||||||||
Db 335 TCGTCGAACGTTCGA 349

RESULT 6
BH816458
LOCUS BH816458 728 bp DNA linear GSS 08-MAY-2002
DEFINITION AM__Ba0021J24f Apis mellifera Apis mellifera genomic clone AM__Ba0021J24f, genomic survey sequence.
ACCESSION BH816458
VERSION BH816458.1 GI:20512115
KEYWORDS. GSS.
SOURCE Apis mellifera (honeybee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
REFERENCE 1 (bases 1 to 728)
AUTHORS Tomkins,J.P., Luo,M., Hunt,G., Main,D., Frisch,D., Page,P.E., Guzman-Nova,E. and Wing,R.A.
TITLE Development of Genomic Resources for honey bee (Apis mellifera L.): BAC Library Construction, Preliminary STC Analysis, and Identification of Clones Associated With Behavioral Traits
JOURNAL Unpublished
COMMENT Contact: Tomkins JP
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: jtmkns@clemson.edu
Total hq bases = 231
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 52
High quality sequence stop: 502.
FEATURES Location/Qualifiers
source 1. .728
/organism="Apis mellifera"
/mol_type="genomic DNA"
/strain="Africanized honey bee"
/db_xref="taxon:7460"
/clone="AM__Ba0021J24f"
/tissue_type="Larva"
/lab_host="E. coli"
/clone_lib="Apis mellifera"
/note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/stc/bee/AM__Ba/ To order clones from this library see http://www.genome.clemson.edu/orders "
BASE COUNT 227 a 134 c 156 g 207 t 4 others
ORIGIN

Query Match 71.4%; Score 15; DB 28; Length 728;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTCGAGATGA 20
||||||||||||||||
Db 118 GAACGTTCGAGATGA 132

RESULT 7
BZ391656/c
LOCUS BZ391656 842 bp DNA linear GSS 30-APR-2003
DEFINITION EINCQ64TR EI_10_12_KB Entamoeba invadens genomic clone EINCQ64, genomic survey sequence.
ACCESSION BZ391656
VERSION BZ391656.1 GI:30238193
KEYWORDS GSS.
SOURCE Entamoeba invadens
ORGANISM Entamoeba invadens
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE 1 (bases 1 to 842)
AUTHORS Loftus,B., Wang,Z., Roncaglia,P., Van Aken,S. and Fraser,C.
TITLE Gene discovery in the Entamoeba invadens genome
JOURNAL Unpublished
COMMENT Other_GSSs: EINCQ64TF
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seq primer: TR
Class: sheared ends.
FEATURES Location/Qualifiers
source 1. .842
/organism="Entamoeba invadens"
/mol_type="genomic DNA"
/strain="IP-1"
/db_xref="taxon:33085"
/clone="EINCQ64"
/clone_lib="EI_10_12_KB"
/note="Vector: pHOS2; Site_1: BstXI; Total genomic DNA was isolated from early log phase trophozoites of E. invadens IP-1 using a Qiagen plant DNA extraction kit. A shotgun medium-size plasmid library (average insert size of 10 - 12 kb) was generated by random mechanical shearing of E. invadens genomic DNA, repairing the ends of DNA fragments with T4 Polymerase, adding BstXI adaptors and ligating into the BstXI site of a pUC-derived vector pHOS2."
BASE COUNT 281 a 152 c 140 g 269 t
ORIGIN

Query Match 71.4%; Score 15; DB 29; Length 842;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTTCGAGATGAT 21
|||||||||||||||
Db 796 AACGTTCGAGATGAT 782

RESULT 8
CD375545/c
LOCUS CD375545 889 bp mRNA linear EST 31-MAY-2003
DEFINITION PTMM00709 Phaeodactylum tricornutum Uni-Zap XR Phaeodactylum tricornutum cDNA 5', mRNA sequence.
ACCESSION CD375545
VERSION CD375545.1 GI:31251159
KEYWORDS EST.
SOURCE Phaeodactylum tricornutum
ORGANISM Phaeodactylum tricornutum
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae; Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
REFERENCE 1 (bases 1 to 889)
AUTHORS Scala,S., Carels,N., Falciatore,A., Chiusano,M.L. and Bowler,C.
TITLE Genome properties of the diatom Phaeodactylum tricornutum
JOURNAL Plant Physiol. 129 (3), 993-1002 (2002)

```
  MEDLINE   22111123
   PUBMED   12114555
COMMENT     Contact: Bowler C
            Laboratory of Molecular Plant Biology
            Stazione Zoologica 'Anton Dohrn'
            Villa Comunale, I-80121, Napoli, Italy
            Tel: 39 081 583 3268/3211
            Fax: 39 081 764 1355
            Email: chris@alpha.szn.it
            Diatom EST Database(http://avesthagen.sznbowler.com)
            Seq primer: T3 backward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .889
                     /organism="Phaeodactylum tricornutum"
                     /mol_type="mRNA"
                     /db_xref="taxon:2850"
                     /cell_line="CCMP632"
                     /clone_lib="Phaeodactylum tricornutum Uni-Zap XR"
                     /note="Vector: Uni-Zap XR vector; Site_1: Eco RI; Site_2:
                     Xho I"
BASE COUNT      216 a    247 c    181 g    214 t     31 others
ORIGIN

  Query Match            71.4%;  Score 15;  DB 14;  Length 889;
  Best Local Similarity  100.0%;  Pred. No. 88;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AACGTTCGAGATGAT 21
              |||||||||||||||
Db        197 AACGTTCGAGATGAT 183


RESULT 9
BX455352/c
LOCUS       BX455352                913 bp    mRNA    linear   EST 22-MAY-2003
DEFINITION  BX455352 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF022YA13 3-PRIME, mRNA sequence.
ACCESSION   BX455352
VERSION     BX455352.1  GI:31019187
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 10667.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAK038CA04NM2&cluster=10667.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAK038CA04NM2.
FEATURES             Location/Qualifiers
     source          1. .913
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF022YA13"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
BASE COUNT      304 a    199 c    163 g    246 t      1 others
ORIGIN

  Query Match            71.4%;  Score 15;  DB 13;  Length 913;
  Best Local Similarity  100.0%;  Pred. No. 88;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db        900 GAACGTTCGAGATGA 886


RESULT 10
CC235774/c
LOCUS       CC235774                1220 bp    DNA     linear   GSS 12-MAY-2003
DEFINITION  CH261-139L19_RM1.2 CH261 Gallus gallus genomic clone CH261-139L19,
            genomic survey sequence.
ACCESSION   CC235774
VERSION     CC235774.1  GI:30562437
KEYWORDS    GSS.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1220)
  AUTHORS   Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
            Warren,W., Graves,T., Mardis,E. and Wilson,R.
  TITLE     Gallus gallus BAC End Reads
  JOURNAL   Unpublished
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 182000   Std Error: 0.00
            Seq primer: RM1 TACGACTCACTATAGGGAGA
            Class: BAC ends
            High quality sequence start: 473
            High quality sequence stop: 541.
FEATURES             Location/Qualifiers
     source          1. .1220
                     /organism="Gallus gallus"
                     /mol_type="genomic DNA"
                     /strain="Red Jungle Fowl"
                     /db_xref="taxon:9031"
                     /clone="CH261-139L19"
                     /sex="female"
                     /cell_line="UCD001, inbred 256"
                     /clone_lib="CH261"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     CH261 Female Chicken library - for library and clone
                     ordering information: http://www.chori.org/bacpac"
BASE COUNT      320 a    330 c    171 g    399 t
ORIGIN

  Query Match            71.4%;  Score 15;  DB 29;  Length 1220;
  Best Local Similarity  100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AACGTTCGAGATGAT 21
              |||||||||||||||
Db        461 AACGTTCGAGATGAT 447


RESULT 11
CNS09N54/c
LOCUS       CNS09N54                108 bp    mRNA    linear   HTC 08-JAN-2003
DEFINITION  Single read from an extremity of a full-length cDNA clone made from
            Anopheles gambiae total adult females. 5-PRIME end of clone
            FK0AAC5AH09 of strain 6-9 of Anopheles gambiae (African malaria
            mosquito).
```

```
ACCESSION   BX066068
VERSION     BX066068.1  GI:27639349
KEYWORDS    HTC.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 108)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
FEATURES             Location/Qualifiers
     source          1. .108
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /strain="6-9"
                     /db_xref="taxon:7165"
                     /clone="FK0AAC5AH09"
                     /plasmid="pME18S-FL"
                     /note="end : 5-PRIME"
BASE COUNT       21 a     31 c     34 g     22 t
ORIGIN

  Query Match            66.7%;  Score 14;  DB 11;  Length 108;
  Best Local Similarity  100.0%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CGAACGTTCGAGAT 18
              ||||||||||||||
Db         61 CGAACGTTCGAGAT 48


RESULT 12
R04873
LOCUS       R04873                   168 bp    mRNA    linear   EST 31-MAR-1995
DEFINITION  pk33h10.r1 Kuwabara Mixed stage C. briggsae Caenorhabditis briggsae
            cDNA, mRNA sequence.
ACCESSION   R04873
VERSION     R04873.1  GI:754609
KEYWORDS    EST.
SOURCE      Caenorhabditis briggsae
  ORGANISM  Caenorhabditis briggsae
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
            ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 168)
  AUTHORS   Hillier,L., Chiapelli,B., Chissoe,S., Clark,N., Couch,J., Dubuque
            ,T., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Kuwabara,P., Le
            ,M., Mardis,E., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan
            ,F., Trevaskis,E., Waterston,R., Wohldmann,P. and Wilson,R.
  TITLE     Washington University Caenorhabditis briggsae EST project
  JOURNAL   Unpublished
COMMENT     Contact: Marra MA
            Washington University Genome Sequencing Center
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1455
            Fax: 314 286 1810
            Email: mmarra@watson.wustl.edu
            PCR_F: TGTAAAACGACGGCCAGTGAGCAAGTTCAGCCTGG
            PCR_B: CAGGAAACAGCTATGACCCTTATGAGTATTTCTTCCAGGGTA
            Source: Washington University Genome Sequencing Center
            PCR amplified DNA is available from Washington University Genome
            Sequencing Center. Aliquots of the library may be requested from P.
            Kuwabara (pek@mrc-lmb.cam.ac.uk).
            Seq primer: Commercially available M13 reverse dye primer.
FEATURES             Location/Qualifiers
     source          1. .168
                     /organism="Caenorhabditis briggsae"
                     /mol_type="mRNA"
                     /strain="G16 Gujarat"
                     /db_xref="taxon:6238"
                     /clone_lib="Kuwabara Mixed stage C. briggsae"
                     /note="Vector: Lambda gt10; Site_1: EcoRI; Site_2: EcoRI;
                     Stage:mixed, Sex:hermaphrodite. Library construction:
                     First strand oligo(dT) primed.  Second strand was as per
                     Gubler/Hoffman.  Ligated to EcoRI adaptors.  Library is
                     non-directional. Library is non-normalized. Library
                     constructed by P.E. Kuwabara.  Additional details on
                     construction of the  library are described in P.E.
                     Kuwabara and S. Shah, NAR 22: 4414 - 4418 (1994). Adaptor
                     sequence: GAATTC CGTTGCTGTCG"
BASE COUNT       46 a     42 c     42 g     38 t
ORIGIN

  Query Match            66.7%;  Score 14;  DB 14;  Length 168;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCG 14
              ||||||||||||||
Db        148 TCGTCGAACGTTCG 161


RESULT 13
AA186214/c
LOCUS       AA186214                 298 bp    mRNA    linear   EST 10-JAN-1997
DEFINITION  T3860 MVAT4 bloodstream form of serodeme WRATat1.1 Trypanosoma
            brucei rhodesiense cDNA 5', mRNA sequence.
ACCESSION   AA186214
VERSION     AA186214.1  GI:1772670
KEYWORDS    EST.
SOURCE      Trypanosoma brucei rhodesiense
  ORGANISM  Trypanosoma brucei rhodesiense
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 298)
  AUTHORS   Djikeng,A., Donelson,J.E. and Majiwa,P.A.O.
  TITLE     Generation of expressed sequence tags as physical landmarks in the
            genome of Trypanosoma brucei
  JOURNAL   Unpublished
COMMENT     Contact: Majiwa PAO
            Molecular Biology Unit
            International Livestock Research Institute
            P.O. Box 30709, Nairobi, Kenya
            Tel: 254-2 630743
            Fax: 254-2 631499
            Email: p.majiwa@cgnet.com
            Seq primer: T3 primer.
FEATURES             Location/Qualifiers
     source          1. .298
                     /organism="Trypanosoma brucei rhodesiense"
                     /mol_type="mRNA"
                     /sub_species="rhodesiense"
                     /db_xref="taxon:31286"
                     /clone_lib="MVAT4 bloodstream form of serodeme WRATat1.1"
                     /note="Vector: Lambda ZAP II (Stratagene); Site_1: EcorI;
                     Site_2: XhoI; The mRNA was purified from a cloned
                     population of bloodstream trypanosomes reexpressing the
                     MVAT4 metacyclic variant surface glycoprotein (VSG). A
                     unidirectional oligo dT-primed EcoRI/XhoI cDNA library was
                     constructed in lambda ZAP II (Stratagene)."
BASE COUNT       93 a     63 c     86 g     56 t
ORIGIN

  Query Match            66.7%;  Score 14;  DB 9;  Length 298;
  Best Local Similarity  100.0%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ACGTTCGAGATGAT 21
              ||||||||||||||
Db        263 ACGTTCGAGATGAT 250
```

```
RESULT 14
CNS09Q90/c
LOCUS       CNS09Q90                348 bp    mRNA    linear   HTC 08-JAN-2003
DEFINITION  Single read from an extremity of a full-length cDNA clone made from
            Anopheles gambiae total adult females. 5-PRIME end of clone
            FK0AAC7AB01 of strain 6-9 of Anopheles gambiae (African malaria
            mosquito).
ACCESSION   BX070096
VERSION     BX070096.1  GI:27643377
KEYWORDS    HTC.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /strain="6-9"
                     /db_xref="taxon:7165"
                     /clone="FK0AAC7AB01"
                     /plasmid="pME18S-FL"
                     /note="end : 5-PRIME"
BASE COUNT       81 a    101 c    114 g     52 t
ORIGIN

  Query Match           66.7%;  Score 14;  DB 11;  Length 348;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CGAACGTTCGAGAT 18
              ||||||||||||||
Db        263 CGAACGTTCGAGAT 250


RESULT 15
BI507844
LOCUS       BI507844                387 bp    mRNA    linear   EST 08-APR-2002
DEFINITION  BB170008B10E04.5 Bee Brain Normalized/Subtracted Library, BB17 Apis
            mellifera cDNA clone BB170008B10E04 5', mRNA sequence.
ACCESSION   BI507844
VERSION     BI507844.1  GI:15358218
KEYWORDS    EST.
SOURCE      Apis mellifera (honeybee)
  ORGANISM  Apis mellifera
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
REFERENCE   1  (bases 1 to 387)
  AUTHORS   Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L.,
            Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
  TITLE     Annotated expressed sequence tags and cDNA microarrays for studies
            of brain and behavior in the honey bee
  JOURNAL   Genome Res. 12 (4), 555-566 (2002)
  MEDLINE   21929762
   PUBMED   11932240
COMMENT     Contact: Gene E. Robinson
            Department of Entomology
            University of Illinois
            505 S. Goodwin Ave., Urbana, IL 61801, USA
            Tel: 217 265 0309
            Fax: 217 244 3499
            Email: generobi@life.uiuc.edu
            This research was funded by the University of Illinois Critical
            Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
            Award in Functional Genomics to G.E. Robinson and an NSF
            Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Plate: BB170008B10  row: E  column: 04
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 387.
FEATURES             Location/Qualifiers
     source          1. .387
                     /organism="Apis mellifera"
                     /mol_type="mRNA"
                     /strain="mixed strains of European bees, predominantly
                     A.m. ligustica"
                     /db_xref="taxon:7460"
                     /clone="BB170008B10E04"
                     /sex="female"
                     /tissue_type="brain"
                     /dev_stage="adult worker honey bee"
                     /lab_host="DH10B"
                     /clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
                     /note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1;
                     Site_2: Not1; This BB17 cDNA library was generated by
                     subtraction of the BB16  library with 4000 previously
                     sequenced clones. The BB16 library was  contributed by the
                     Soares laboratory and it was constructed and  normalized
                     as described by Bonaldo, M.F., Lennon, G. and  Soares,
                     M.B. (1996), Genome Research 6(9): 791-806. RNA was
                     prepared  from dissected brains of adult worker bees of
                     various ages and  various behavioral groups. "
BASE COUNT      125 a     71 c     95 g     96 t
ORIGIN

  Query Match           66.7%;  Score 14;  DB 12;  Length 387;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ACGTTCGAGATGAT 21
              ||||||||||||||
Db        228 ACGTTCGAGATGAT 241


Search completed: December 19, 2003, 13:40:52
Job time : 1316 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:58:44 ; Search time 1195 Seconds
(without alignments)
718.914 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	21	6	AX592442	AX592442 Sequence
2	19	90.5	19	6	AX592329	AX592329 Sequence
3	19	90.5	22	6	AX592340	AX592340 Sequence
4	16	76.2	18	6	AX592324	AX592324 Sequence
5	16	76.2	119972	2	AP004029	AP004029 Oryza sat
c 6	16	76.2	126038	8	AP000367	AP000367 Oryza sat
7	16	76.2	144952	2	AP005629	AP005629 Oryza sat
c 8	16	76.2	146568	2	AC141727	AC141727 Apis mell
c 9	16	76.2	166304	2	AC130730	AC130730 Oryza sat
10	15	71.4	22	6	AR268334	AR268334 Sequence
11	15	71.4	22	6	AR287741	AR287741 Sequence
12	15	71.4	22	6	AR287743	AR287743 Sequence
13	15	71.4	22	6	AR308057	AR308057 Sequence
14	15	71.4	22	6	AX036945	AX036945 Sequence
15	15	71.4	22	6	AX046993	AX046993 Sequence
16	15	71.4	22	6	AX083675	AX083675 Sequence
17	15	71.4	22	6	AX083676	AX083676 Sequence
18	15	71.4	22	6	AX135650	AX135650 Sequence
19	15	71.4	22	6	AX148636	AX148636 Sequence
20	15	71.4	22	6	AX148637	AX148637 Sequence
21	15	71.4	22	6	AX250701	AX250701 Sequence
22	15	71.4	22	6	AX250702	AX250702 Sequence
23	15	71.4	22	6	AX252291	AX252291 Sequence
24	15	71.4	22	6	AX252292	AX252292 Sequence
25	15	71.4	22	6	AX252509	AX252509 Sequence
26	15	71.4	22	6	AX252510	AX252510 Sequence
27	15	71.4	22	6	AX252520	AX252520 Sequence
28	15	71.4	22	6	AX252521	AX252521 Sequence
29	15	71.4	22	6	AX252934	AX252934 Sequence
30	15	71.4	22	6	AX252935	AX252935 Sequence
31	15	71.4	22	6	AX253113	AX253113 Sequence
32	15	71.4	22	6	AX253114	AX253114 Sequence
33	15	71.4	22	6	AX253123	AX253123 Sequence
34	15	71.4	22	6	AX253124	AX253124 Sequence
35	15	71.4	22	6	AX468499	AX468499 Sequence
36	15	71.4	22	6	AX592312	AX592312 Sequence
37	15	71.4	22	6	AX592322	AX592322 Sequence
38	15	71.4	22	6	AX592332	AX592332 Sequence
39	15	71.4	22	6	AX592350	AX592350 Sequence
40	15	71.4	22	6	AX592355	AX592355 Sequence
41	15	71.4	22	6	AX592356	AX592356 Sequence
42	15	71.4	22	6	AX592369	AX592369 Sequence
43	15	71.4	22	6	AX720306	AX720306 Sequence
44	15	71.4	22	6	BD009235	BD009235 Immunosti
45	15	71.4	22	6	BD182369	BD182369 Anti-tumo

ALIGNMENTS

RESULT 1
AX592442
LOCUS AX592442 21 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 132 from Patent WO02052002.
ACCESSION AX592442
VERSION AX592442.1 GI:27950544
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 132 04-JUL-2002;
Dynavax Technologies Corporation (US)

```
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
BASE COUNT        5 a      4 c      6 g      6 t
ORIGIN

  Query Match             100.0%;  Score 21;  DB 6;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATGAT 21
              |||||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATGAT 21


RESULT 2
AX592329
LOCUS       AX592329                 19 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 19 from Patent WO02052002.
ACCESSION   AX592329
VERSION     AX592329.1  GI:27950431
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 19 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
BASE COUNT        4 a      4 c      6 g      5 t
ORIGIN

  Query Match             90.5%;  Score 19;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          1 TCGTCGAACGTTCGAGATG 19


RESULT 3
AX592340
LOCUS       AX592340                 22 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 30 from Patent WO02052002.
ACCESSION   AX592340
VERSION     AX592340.1  GI:27950442
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 30 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
BASE COUNT        5 a      4 c      7 g      6 t
ORIGIN

  Query Match             90.5%;  Score 19;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          4 TCGTCGAACGTTCGAGATG 22


RESULT 4
AX592324
LOCUS       AX592324                 18 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 14 from Patent WO02052002.
ACCESSION   AX592324
VERSION     AX592324.1  GI:27950426
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fearon,K.L. and Dina,D.
  TITLE     Immunomodulatory polynucleotides and methods of using the same
  JOURNAL   Patent: WO 02052002-A 14 04-JUL-2002;
            Dynavax Technologies Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide containing CG"
BASE COUNT        4 a      4 c      5 g      5 t
ORIGIN

  Query Match             76.2%;  Score 16;  DB 6;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCGAACGTTCGAGATG 19
              ||||||||||||||||
Db          3 TCGAACGTTCGAGATG 18


RESULT 5
AP004029
LOCUS       AP004029             119972 bp    DNA     linear   HTG 21-MAR-2002
DEFINITION  Oryza sativa (japonica cultivar-group) chromosome 2 clone
            OJ1136_D07, *** SEQUENCING IN PROGRESS ***.
ACCESSION   AP004029
VERSION     AP004029.1  GI:15130691
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
            clone:OJ1136_D07
  JOURNAL   Published Only in Database (2001)
REFERENCE   2  (bases 1 to 119972)
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2001) Takuji Sasaki, National Institute of
            Agrobiological Resources, Rice Genome Research Program; Kannondai
            2-1-2, Tsukuba, Ibaraki 305-8602, Japan
            (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
            Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT     The nucleotide sequence of this BAC clone was generated by
            combining Monsanto and RGP-Japan sequencing data.
            NOTE: It currently consists of 1 contigs. Gaps between the contigs
```

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          are represented as runs of N. The order of the pieces is believed
          to be correct as given, however the sizes of the gaps between them
          are based on estimates that have provided by the submitter. This
          sequence will be replaced by the finished sequence as soon as it is
          available and the accession number will be preserved.
          * NOTE: This is a 'working draft' sequence.
          * This sequence will be replaced
          * by the finished sequence as soon as it is available and
          * the accession number will be preserved.
FEATURES             Location/Qualifiers
     source          1. .119972
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="genomic DNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /chromosome="2"
                     /clone="OJ1136_D07"
BASE COUNT    34735 a  25005 c  25414 g  34818 t
ORIGIN

  Query Match             76.2%;  Score 16;  DB 2;  Length 119972;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CGAACGTTCGAGATGA 20
              ||||||||||||||||
Db      38384 CGAACGTTCGAGATGA 38399


RESULT 6
AP000367/c
LOCUS       AP000367              126038 bp    DNA     linear   PLN 21-MAR-2002
DEFINITION  Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,
            clone:P0437H03 (contig b).
ACCESSION   AP000367
VERSION     AP000367.1  GI:5441876
KEYWORDS    .
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Oryza sativa Nipponbare(GA3) genomic DNA, chromosome 2, PAC
            clone:P0437H03 (contig b)
  JOURNAL   Published Only in Database (1999)
REFERENCE   2  (bases 1 to 126038)
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUL-1999) Takuji Sasaki, National Institute of
            Agrobiological Resources, Rice Genome Research Program; Kannondai
            2-1-2, Tsukuba, Ibaraki 305-8602, Japan
            (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
            Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT     This PAC clone has 10 kbp sequence gap, which result in 2 contigs
            (contig a, b). This sequence shows contig b. The orientation of the
            sequence is from SP6 to T7 of the PAC clone. Genes were predicted
            from the integrated results of the following:GENSCAN1.0, BLASTN1.4,
            BLASTX2.0 as well as SlicePredictor (October1998 version). The
            genomic sequence was searched against the non-redundant database
            NRP(PIR,SWISSPROT, GENPEPT, PDB) from MAFF DNAbank and the cDNA
            sequence database at RGP. Protein similarities of the cording
            regions were searched against NRP with BLASTP2.0. ESTs represent
            the identified cDNA sequences using BLASTN1.4 with the
            corresponding DDBJ accession no. and RGP clone ID.
FEATURES             Location/Qualifiers
     source          1. .126038
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="genomic DNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /chromosome="2"
                     /clone="P0437H03 (contig b)"
     CDS             complement(join(1542. .1704,1808. .2005,2133. .2332,
                     2428. .2541,2732. .2868,3006. .3116,5410. .5554))
                     /note="Similar to glycogenin glucosyltransferase (EC
                     2.4.1.186). (Z97341)"
                     /codon_start=1
                     /protein_id="BAA82375.1"
                     /db_xref="GI:5441877"
                     /translation="MKHGYVRECEYVAIFDADFQPDPDFLRRTIPFLVHNSDIALVQA
                     RWRFVNADECLMTRMQEMSLDYHFTVEQEVSSSVCAFFGFNGTAGVWRVSAVNEAGGW
                     KDRTTVEDMDLAIRASLKGWKFVYLGDVQVKSELPSTFKAFRFQQHRWSCGPANLFRK
                     MLMEIVRNKKVTIWKKIHVIYNFFLIRKIIAHIVTFAFYCLIIPATIFVPEVRIPKWG
                     CVYIPTIITLLNSVGTPRSFHLLFFWILFENVMSLHRTKATLIGLLEAGRANEWVVTE
                     KLGNALKMKSSSKSSAKKSFMRVWDRLNVTELGVAAFLFSCGWYDLAFGKDHFFIYLF
                     FQGAAFFIVGIGYVGTIVPQS"
     CDS             join(9281. .9351,11606. .11736,12883. .12994,13030. .13164,
                     13319. .13331)
                     /note="hypothetical protein"
                     /codon_start=1
                     /protein_id="BAA82376.1"
                     /db_xref="GI:5441878"
                     /translation="MNKEQQGKSIFTMGGWDLTSYNTLSDPASKKPSVAQVNCKCKFS
                     QCVVQFMETPRVDVEYSLLQQLPLIDTAFLCRKGIDLKKTSRDEHDLRKVTPVYTTIR
                     CTGHEAVLLLLVLRFGSSLSESLARFARTKVCSDSSECDDDDDDSGDESNS"
     CDS             complement(16578. .17255)
                     /note="ESTs AU070372(S13446),AU075541(S0353) correspond to
                     a region of the predicted gene.
                     Similar to Arabidopsis thaliana BAC genomic sequence.
                     (AC002292)"
                     /codon_start=1
                     /protein_id="BAA82377.1"
                     /db_xref="GI:5441879"
                     /translation="MAAPTAAALSTLSTASVTSGKRFITSSFSLSFSSRPLATGVRAA
                     GARAARRSAASASTVVATIAVGDKLPDATLSYFDPADGELKTVTVAELTAGRKAVLFA
                     VPGAFTPTCSQKHLPGFIEKAGELHAKGVDAIACVSVNDAFVMRAWKESLGLGDADVL
                     LLSDGNLELTRALGVEMDLSDKPMGLGVRSRRYALLADDGVVKVLNLEEGGAFTTSSA
                     EEMLKAL"
     LTR             complement(17699. .18004)
                     /note="3' long terminal repeat"
     CDS             complement(join(18782. .19019,19135. .19266,19513. .19610,
                     19855. .20113,20190. .20488,21053. .21389,21495. .21645,
                     22169. .22484,22743. .22774,23219. .24224))
                     /note="EST C28952(C62945) corresponds to a region of the
                     predicted gene.
                     Similar to maize transposon MuDR mudrA protein.
                     (AC003981)"
                     /codon_start=1
                     /protein_id="BAA82378.1"
                     /db_xref="GI:5441880"
                     /translation="MADEGERVGIIVDEMEREDSDNEEVDDDASSDEEGDVMATDWAN
                     EDFSGLVISEGDHVPWEYKENEVIEGARYAHKDERKEAVKHWAVSLQREFRVVKSTNY
                     VYEVRCMKEDCPWRVHAYKGKWNDYWKVSIVTEHKCYLQGVEKYHRNITSAFVASEMY
                     SSVVGNIGFEPKSIIRHIENKFKYTISYAKAWRAKQKIIEMRYGTFEASYDNLPRLLA
                     TIAQRNNNTYYDLHTFTSVDDRTKSVLQRAFFSLGACINAFVHCRPVLCIDGTFMTGK
                     YRGQILTAIGCDGNNQVLPMAFAFVESENTESWYWFLERVHIAVVCMRPNVCLIHDRH
                     AEVYNWVMRGVRECVLKADGGCTCSCMKPKLHHLPCSHVLAAAGDCGISPNVYVSNYF
                     RKEAIFHTWSEEIYGFGISGSYTTLSAQVFYIPDPSKLRVKKGRRQTRRIRNDMDESE
                     AGMAYDTPALLNRGIDRNHRSFLSAVEGAQLGTFRPRTSREWLRVDPRHVPWLVEAAA
                     DDRDPAKRWDADRSLLAALVDRWRPETHTFHLPCGEMAPTLQDVSYLLGLPLAGAAVG
                     PVDGVFGWKEDITARFEQVMRLPHLGPTTTLPPYSTVGPSKAWLLQFTRRYAHVQVRR
                     GYPDFVFEFDRLQPSDVIWEPYTEEAVAARAPLGLSSLCTRDQAYWLTILPMVFDIFV
                     EPHCPQRVMRQFGLRQVFPGNVQPTVLPADHSLTRRGQLAGALWAPRVQQYVDDWVLA
                     TEEVINELFPHTEENYRDYLRWYLPRTRARVTFTPDAPEPHVAAVTDAYPTHRDRDYF
                     VARCGRRTSSWSGTTTASRAYRRSRTSTYGTYFARTSSAFERVRRHDRRFHELRRGVR
                     HLFGRVRQLFLSRSVDPSPTRTGPTSQFYDDDLHGADHHDVLGSSQLGGAPEAHTQEQ
                     PEVTPVQAGRVGRAVPPDRLTYSHGHIRAQGRRDRGKRPRQ"
     LTR             complement(25215. .25521)
                     /note="5' long terminal repeat"
     CDS             join(25810. .25825,29004. .31165)
                     /note="Similar to putative receptor kinase. (AC002332)"
                     /codon_start=1
                     /protein_id="BAA82379.1"
                     /db_xref="GI:5441881"
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                     /organism="Apis mellifera"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7460"
                     /clone="CH224-57G3"
BASE COUNT    39316 a  30537 c  30943 g  39489 t   6283 others
ORIGIN

  Query Match          76.2%;  Score 16;  DB 2;  Length 146568;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CGTCGAACGTTCGAGA 17
              ||||||||||||||||
Db     135270 CGTCGAACGTTCGAGA 135255


RESULT 9
AC130730/c
LOCUS       AC130730               166304 bp    DNA     linear   HTG 14-AUG-2002
DEFINITION  Oryza sativa (japonica cultivar-group) chromosome 5 clone P0681D04,
            *** SEQUENCING IN PROGRESS ***, 6 ordered pieces.
ACCESSION   AC130730
VERSION     AC130730.1  GI:22218364
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 166304)
  AUTHORS   Chow,T.-Y., Hsing,Y.-I.C., Chen,C.-S., Chen,H.-H., Liu,S.-M.,
            Chao,Y.-T., Chang,S.-J., Chen,H.-C., Chen,S.-K., Chen,T.-R.,
            Chen,Y.-L., Cheng,C.-H., Chung,C.-I., Han,S.-Y., Hsiao,S.-H.,
            Hsiung,J.-N., Hsu,C.-H., Huang,J.-J., Kau,P.-I., Lee,M.-C.,
            Leu,H.-L., Li,Y.-F., Lin,S.-J., Lin,Y.-C., Wu,S.-W., Yu,C.-Y.,
            Yu,S.-W., Wu,H.-P. and Shaw,J.-F.
  TITLE     Oryza sativa PAC P0681D04 genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 166304)
  AUTHORS   Chow,T.-Y. and Hsing,Y.-I.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-AUG-2002) Institute of Botany, Academia Sinica, 128,
            Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
COMMENT     * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1     8678: contig of 8678 bp in length
            *     8679     8778: gap of unknown length
            *     8779    14903: contig of 6125 bp in length
            *    14904    15003: gap of unknown length
            *    15004    35393: contig of 20390 bp in length
            *    35394    35493: gap of unknown length
            *    35494   121324: contig of 85831 bp in length
            *   121325   121424: gap of unknown length
            *   121425   135356: contig of 13932 bp in length
            *   135357   135456: gap of unknown length
            *   135457   166304: contig of 30848 bp in length.
FEATURES             Location/Qualifiers
     source          1. .166304
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="genomic DNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /chromosome="5"
                     /clone="P0681D04"
BASE COUNT    46182 a  37272 c  36481 g  45869 t    500 others
ORIGIN

  Query Match          76.2%;  Score 16;  DB 2;  Length 166304;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CGAACGTTCGAGATGA 20
              ||||||||||||||||
Db      99712 CGAACGTTCGAGATGA 99697


RESULT 10
AR268334
LOCUS       AR268334               22 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 19 from patent US 6498148.
ACCESSION   AR268334
VERSION     AR268334.1  GI:29698684
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E.
  TITLE     Immunization-free methods for treating antigen-stimulated
            inflammation in a mammalian host and shifting the host's antigen
            immune responsiveness to a Th1 phenotype
  JOURNAL   Patent: US 6498148-A 19 24-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
BASE COUNT        6 a      3 c      7 g      6 t
ORIGIN

  Query Match          71.4%;  Score 15;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              ||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 11
AR287741
LOCUS       AR287741               22 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6534062.
ACCESSION   AR287741
VERSION     AR287741.1  GI:31674761
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E., Cho,H.J., Richman,D. and Horner,A.A.
  TITLE     Methods for increasing a cytotoxic T lymphocyte response in vivo
  JOURNAL   Patent: US 6534062-A 1 18-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
BASE COUNT        6 a      3 c      7 g      6 t
ORIGIN

  Query Match          71.4%;  Score 15;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              ||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 12
AR287743
LOCUS       AR287743               22 bp    DNA     linear   PAT 12-JUN-2003
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DEFINITION  Sequence 3 from patent US 6534062.
ACCESSION   AR287743
VERSION     AR287743.1  GI:31674763
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E., Cho,H.J., Richman,D. and Horner,A.A.
  TITLE     Methods for increasing a cytotoxic T lymphocyte response in vivo
  JOURNAL   Patent: US 6534062-A 3 18-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
BASE COUNT        6 a      3 c      7 g      6 t
ORIGIN

  Query Match             71.4%;  Score 15;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 13
AR308057
LOCUS       AR308057                 22 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6552006.
ACCESSION   AR308057
VERSION     AR308057.1  GI:31698950
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E., Kornbluth,R., Catanzaro,A., Hayashi,T. and Carson,D.
  TITLE     Immunomodulatory polynucleotides in treatment of an infection by an
            intracellular pathogen
  JOURNAL   Patent: US 6552006-A 1 22-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
BASE COUNT        6 a      3 c      7 g      6 t
ORIGIN

  Query Match             71.4%;  Score 15;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 14
AX036945
LOCUS       AX036945                 22 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 2 from Patent FR2790955.
ACCESSION   AX036945
VERSION     AX036945.1  GI:11226373
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Carpentier,A.
  JOURNAL   Patent: FR 2790955-A 2 22-SEP-2000;
            ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="oligodesoxynucleotide"
BASE COUNT        6 a      3 c      7 g      6 t
ORIGIN

  Query Match             71.4%;  Score 15;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 15
AX046993
LOCUS       AX046993                 22 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 2 from Patent WO0067787.
ACCESSION   AX046993
VERSION     AX046993.1  GI:11876420
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Moss,R.B.
  TITLE     Hiv immunogenic compositions and methods
  JOURNAL   Patent: WO 0067787-A 2 16-NOV-2000;
            THE IMMUNE RESPONSE CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="phosphorothioate-modified synthetic
                     oligodeoxynucleotide"
BASE COUNT        6 a      3 c      7 g      6 t
ORIGIN

  Query Match             71.4%;  Score 15;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


Search completed: December 19, 2003, 13:18:52
Job time : 1199 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:58:44 ; Search time 147 Seconds
(without alignments)
385.634 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgtcgaacgttcgagatgat 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	21	24	ABQ75182	ISS immunomodulato
2	19	90.5	19	24	ABQ75170	ISS immunomodulato
3	19	90.5	22	24	ABQ75181	ISS immunomodulato
4	16	76.2	18	24	ABQ75165	ISS immunomodulato
5	15	71.4	20	24	AAD24905	Double-stranded im
6	15	71.4	22	19	AAV32079	Nucleotide sequenc
7	15	71.4	22	20	AAX36624	ISS-ODN DY1018 nuc
c 8	15	71.4	22	20	AAV80105	Oligo used in expe
9	15	71.4	22	20	AAV80096	Immunomodulatory o
10	15	71.4	22	20	AAV80097	Immunomodulatory o
11	15	71.4	22	20	AAV80102	Immunomodulatory o
12	15	71.4	22	20	AAV80103	Immunomodulatory o
13	15	71.4	22	21	AAC64051	Immunostimulatory
14	15	71.4	22	21	AAA96253	Sequence of a stab
15	15	71.4	22	21	AAA90458	CpG adjuvant oligo
16	15	71.4	22	21	AAA14467	Immunostimulatory
17	15	71.4	22	21	AAA38065	Immunostimulatory
18	15	71.4	22	21	AAA38066	Immunostimulatory
19	15	71.4	22	21	AAA38071	Immunostimulatory
20	15	71.4	22	21	AAA38072	Immunostimulatory
21	15	71.4	22	21	AAZ55876	Immunomodulatory o
22	15	71.4	22	22	AAH43338	Immunomodulatory p
23	15	71.4	22	22	AAS14664	Immunostimulatory
24	15	71.4	22	22	AAS14665	Immunostimulatory
25	15	71.4	22	22	AAH75992	Immunomodulatory o
26	15	71.4	22	22	AAH75993	Immunomodulatory o
27	15	71.4	22	22	AAH42533	Phosphorothioate b
28	15	71.4	22	22	AAH73439	Immunomodulatory n
29	15	71.4	22	22	AAH44109	5' terminal NH2 gr
30	15	71.4	22	22	AAH41573	Immunostimulatory
31	15	71.4	22	22	AAH41574	Immunostimulatory
32	15	71.4	22	22	AAH20403	CpG motif containi
33	15	71.4	22	22	AAF77040	Immunomodulatory D
34	15	71.4	22	22	AAF77041	Immunostimulatory
35	15	71.4	22	22	AAF29800	Cholera toxin immu
36	15	71.4	22	22	AAC82107	Oligonucleotide OD
37	15	71.4	22	22	AAA92377	CG motif and CFA c
38	15	71.4	22	24	ABV73190	Nucleotide sequenc
39	15	71.4	22	24	ABQ78627	ISS enhancing HIV-
40	15	71.4	22	24	AAL44504	CpG motif oligonuc
41	15	71.4	22	24	ABQ75153	ISS immunomodulato
42	15	71.4	22	24	ABQ75163	ISS immunomodulato
43	15	71.4	22	24	ABQ75173	ISS immunomodulato
44	15	71.4	22	24	ABQ75206	ISS immunomodulato
45	15	71.4	22	24	ABQ75211	ISS immunomodulato

ALIGNMENTS

RESULT 1
ABQ75182
ID ABQ75182 standard; DNA; 21 BP.
XX
AC ABQ75182;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:132.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US50821.
XX
PR 27-DEC-2000; 2000US-258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX

DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence -
XX
PS Claim 4; Page 21; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from
CC the present invention.
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 21; DB 24; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATGAT 21
||||||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATGAT 21

RESULT 2
ABQ75170
ID ABQ75170 standard; DNA; 19 BP.
XX
AC ABQ75170;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:19.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US50821.
XX
PR 27-DEC-2000; 2000US-258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence -
XX
PS Claim 4; Page 20; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from
CC the present invention.
XX
SQ Sequence 19 BP; 4 A; 4 C; 6 G; 5 T; 0 other;

Query Match 90.5%; Score 19; DB 24; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTCGAGATG 19
|||||||||||||||||||
Db 1 TCGTCGAACGTTCGAGATG 19

RESULT 3
ABQ75181
ID ABQ75181 standard; DNA; 22 BP.
XX
AC ABQ75181;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:30.
XX
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US50821.
XX
PR 27-DEC-2000; 2000US-258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX

PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence -
XX
PS Disclosure; Page 21; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from
CC the present invention.
XX
SQ Sequence 22 BP; 5 A; 4 C; 7 G; 6 T; 0 other;

Query Match 90.5%; Score 19; DB 24; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TCGTCGAACGTTCGAGATG 19
              |||||||||||||||||||
Db          4 TCGTCGAACGTTCGAGATG 22
```

RESULT 4
ABQ75165
ID ABQ75165 standard; DNA; 18 BP.
XX
AC ABQ75165;
XX
DT 05-NOV-2002 (first entry)
XX
DE ISS immunomodulatory oligonucleotide SEQ ID NO:14.
XX
KW Immunostimulatory sequence; ISS; immunomodulatory; immune response;
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KW virucide; antibacterial; protozoacide; ss.
XX
OS Synthetic.
XX
PN WO200252002-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-US50821.
XX
PR 27-DEC-2000; 2000US-258675P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Fearon KL, Dina D;
XX
DR WPI; 2002-657426/70.
XX
PT Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence -
XX
PS Example 1; Page 20; 95pp; English.
XX
CC The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (I); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory oligonucleotide from
CC the present invention.
XX
SQ Sequence 18 BP; 4 A; 4 C; 5 G; 5 T; 0 other;

Query Match 76.2%; Score 16; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 TCGAACGTTCGAGATG 19
              ||||||||||||||||
Db          3 TCGAACGTTCGAGATG 18
```

RESULT 5
AAD24905
ID AAD24905 standard; DNA; 20 BP.
XX
AC AAD24905;
XX
DT 12-MAR-2002 (first entry)
XX
DE Double-stranded immunostimulatory oligodeoxynucleotide (ISS-ODN).
XX
KW Cell death; DNA damage; DNA-dependent protein kinase; DNA-PK; necrosis;
KW immune response; apoptosis; Alzheimer's disease; Parkinson's disease;
KW rheumatoid arthritis; inflammation; osteoporosis; myocardial infarction;
KW liver disease; reperfusion injury; carcinoma; multiple sclerosis; stroke;
KW amyotrophic lateral sclerosis; Acquired Immune Deficiency Syndrome; AIDS;
KW head injury damage; aplastic anaemia; tumour; organ transplantation;
KW cerebral infarction; follicular lymphomas; systemic lupus erythematosus;
KW viral infection; glomerulonephritis; apoptosis; autoimmune disorder;
KW sepsis; immunostimulatory oligodeoxynucleotide; ISS-ODN; ds.
XX
OS Unidentified.
XX
PN WO200185910-A2.
XX
PD 15-NOV-2001.
XX
PF 04-MAY-2001; 2001WO-US14508.
XX
PR 05-MAY-2000; 2000US-202274P.
PR 17-JAN-2001; 2001US-262321P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Raz E, Lois AF, Takabayashi K;
XX

DR WPI; 2002-062244/08.
XX
PT Modulating cell death or reducing DNA damage in eukaryotic cells,
PT useful for reducing cell death in individual or organ, comprises
PT contacting cell with agent modulating biological activity of
PT DNA-dependent protein kinase -
XX
PS Example 1; Page 31; 57pp; English.
XX
CC The invention relates to a method for modulating cell death or reducing
CC DNA damage in an eukaryotic cell by contacting the cell with an agent
CC that modulates the biological activity of DNA-dependent protein kinase
CC (DNA-PK). The invention also relates nucleic acids which modulate the
CC immune response binding to Ku antigen, resulting in activation of DNA-PK.
CC The method is useful for modulating cell death or reducing DNA damage in
CC an eukaryotic cell, for treating any disorder resulting from a genotoxic
CC insert to a cell e.g., necrosis, apoptosis. The method is also useful
CC for treating cell death-related indications such as Alzheimer's disease,
CC Parkinson's disease, rheumatoid arthritis, septic shock, sepsis, stroke,
CC central nervous system inflammation, osteoporosis, degenerative liver
CC disease, cerebellar degeneration, reperfusion injury, multiple sclerosis,
CC amyotrophic lateral sclerosis, myocardial infarction, head injury damage,
CC acquired immunodeficiency syndrome (AIDS), aplastic anaemia, cerebral
CC infarction, bypass heart surgery, organ transplantation. The method is
CC also useful for treating follicular lymphomas, carcinomas, autoimmune
CC disorders (systemic lupus erythematosus), hormone dependent tumours,
CC immune mediated glomerulonephritis; apoptosis and viral infections. The
CC present sequence is immunostimulatory oligodeoxynucleotide (ISS-ODN)
CC used for identifying ISS-binding protein, which is used in the
CC exemplification of the invention.
XX
SQ Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 other;

Query Match 71.4%; Score 15; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTCGAGATGA 20
||||||||||||||||
Db 6 GAACGTTCGAGATGA 20

RESULT 6
AAV32079
ID AAV32079 standard; DNA; 22 BP.
XX
AC AAV32079;
XX
DT 09-SEP-1998 (first entry)
XX
DE Nucleotide sequence of DY1018.
XX
KW DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;
KW immunisation; anaphylaxis; IgE; retinopathies; ss.
XX
OS synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..22
FT /*tag= a
FT /note= "phosphothioate backbone"
XX
PN WO9816247-A1.
XX
PD 23-APR-1998.
XX
PF 09-OCT-1997; 97WO-US19004.
XX
PR 11-OCT-1996; 96US-0028118.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Carson DA, Raz E, Roman M;
XX
DR WPI; 1998-261028/23.
XX
PT New immunomodulatory compositions - comprising an antigen conjugated
PT to a polynucleotide that contains an immunostimulatory sequence
XX
PS Example 1; Page 36; 69pp; English.
XX
CC This is the nucleotide sequence of DY1018, which is conjugated to
CC beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule
CC (IMM), which comprises an antigen conjugated to a polynucleotide
CC (PN) that contains at least one immunostimulatory nucleotide sequence
CC (ISS). The conjugate synergistically boost the magnitude of the host
CC immune response against an antigen to a level greater that the host
CC immune response to either the IMM, antigen or ISS-PN alone. These
CC responses to ISS-PN/IMM conjugates are particularly acute during
CC the important early phase of the host immune response to an antigen.
CC The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular
CC (Th1 type) immune responses of the host. Thus, use of the method to
CC boost the immune responsiveness of a host to subsequent challenge by a
CC sensitising antigen without immunisation avoids the risk of
CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE
CC production in response to the antigen challenge. The conjugates can
CC also be used to combat pathogenic infection and to stimulate
CC therapeutic angiogenesis to treat conditions in which localised blood
CC flow plays a significant etiological role, e.g. retinopathies.
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 19; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTCGAGATGA 20
||||||||||||||||
Db 8 GAACGTTCGAGATGA 22

RESULT 7
AAX36624
ID AAX36624 standard; DNA; 22 BP.
XX
AC AAX36624;
XX
DT 09-JUL-1999 (first entry)
XX
DE ISS-ODN DY1018 nucleotide sequence.
XX
KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;
KW granulocyte-mediated tissue inflammation; Th2 type immune response;
KW immune responsiveness modulation; idiopathic hypereosiniphilic syndrome;
KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;
KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;
KW eosinophilic fasciitis; therapy; ss.
XX
OS Synthetic.
XX
PN WO9911275-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18382.
XX
PR 05-SEP-1997; 97US-0927120.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Ray E;
XX
DR WPI; 1999-312404/26.
XX
PT Reducing antigen-stimulated granulocyte-mediated inflammation
XX

PS Example 2; Page 30; 69pp; English.
XX
CC This is the ISS-ODN DY1018 nucleotide sequence.
CC The invention relates to a method for preventing or reducing
CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,
CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:
CC (a) reduction in, or the absence of, a Th2 type immune response is
CC measured; or (b) there is a reduction or absence of other clinical signs
CC of inflammation in the host after antigen challenge. The method is used
CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,
CC and to modulate the host's immune responsiveness to an antigen,
CC particularly where the subject suffers from asthma, nasal polyposis,
CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,
CC eosinophilic fasciitis, idiopathic hypereosiniphilic syndrome, or
CC cutaneous basophil hypersensitivity. Unlike prior art treatment by
CC antigen immunisation, the method is an antigen-independent method,
CC and avoids host production of both interleukin-4 (IL-4), which carries
CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte
CC adhesion to endothelia.
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTCGAGATGA 20
||||||||||||||||
Db 8 GAACGTTCGAGATGA 22

RESULT 8
AAV80105/c
ID AAV80105 standard; DNA; 22 BP.
XX
AC AAV80105;
XX
DT 12-MAR-1999 (first entry)
XX
DE Oligo used in experiments for stimulation of cytokine production.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11578.
XX
PR 06-JUN-1997; 97US-0048793.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Dina D, Roman M, Schwartz D;
XX
DR WPI; 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases
XX
PS Example 1; Page 29; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent
CC oligonucleotides that were tested for immunostimulatory activity. These
CC were used in experiments for the stimulation of cytokine production and
CC were found to lack immunostimulatory activity. The invention provides
CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.
XX
SQ Sequence 22 BP; 5 A; 7 C; 4 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTCGAGATGA 20
||||||||||||||||
Db 15 GAACGTTCGAGATGA 1

RESULT 9
AAV80096
ID AAV80096 standard; DNA; 22 BP.
XX
AC AAV80096;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11578.
XX
PR 06-JUN-1997; 97US-0048793.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Dina D, Roman M, Schwartz D;
XX
DR WPI; 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases
XX
PS Claim 7; Page 29; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased

```
CC   cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC   specific claimed examples of such immunomodulatory oligonucleotides.
XX
SQ   Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

  Query Match            71.4%;  Score 15;  DB 20;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 19;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 10
AAV80097
ID   AAV80097 standard; DNA; 22 BP.
XX
AC   AAV80097;
XX
DT   12-MAR-1999  (first entry)
XX
DE   Immunomodulatory oligo comprising an ISS sequence.
XX
KW   Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW   ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW   human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW   B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS   Synthetic.
XX
PN   WO9855495-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998;   98WO-US11578.
XX
PR   06-JUN-1997;   97US-0048793.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Dina D,  Roman M,  Schwartz D;
XX
DR   WPI; 1999-059898/05.
XX
PT   Immunostimulatory oligonucleotides regulate the immune system - and
PT   contain an immune-stimulating octanucleotide sequence; for treating
PT   cancer, allergic and infectious diseases
XX
PS   Claim 5; Page 29; 63pp; English.
XX
CC   The invention relates to immunomodulatory oligonucleotides that comprise
CC   at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC   sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC   GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC   patients needing immune regulation, such as those suffering from cancer,
CC   an allergic disease and asthma. They are also used to prevent infectious
CC   diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC   and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC   Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC   Schistosoma. The immunomodulatory sequences are used to screen for human
CC   immunostimulatory activity by incubating macrophage cells and the
CC   oligonucleotide; and determining the relative amount of Th1-biased
CC   cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC   specific claimed examples of such immunomodulatory oligonucleotides.
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

  Query Match            71.4%;  Score 15;  DB 20;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 19;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 11
AAV80102
ID   AAV80102 standard; DNA; 22 BP.
XX
AC   AAV80102;
XX
DT   12-MAR-1999  (first entry)
XX
DE   Immunomodulatory oligo comprising an ISS sequence.
XX
KW   Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW   ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW   human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW   B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    11
FT                    /*tag=  a
FT                    /note= "5-bromocytosine"
XX
PN   WO9855495-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998;   98WO-US11578.
XX
PR   06-JUN-1997;   97US-0048793.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Dina D,  Roman M,  Schwartz D;
XX
DR   WPI; 1999-059898/05.
XX
PT   Immunostimulatory oligonucleotides regulate the immune system - and
PT   contain an immune-stimulating octanucleotide sequence; for treating
PT   cancer, allergic and infectious diseases
XX
PS   Claim 23; Page 30; 63pp; English.
XX
CC   The invention relates to immunomodulatory oligonucleotides that comprise
CC   at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC   sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC   GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC   patients needing immune regulation, such as those suffering from cancer,
CC   an allergic disease and asthma. They are also used to prevent infectious
CC   diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC   and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC   Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC   Schistosoma. The immunomodulatory sequences are used to screen for human
CC   immunostimulatory activity by incubating macrophage cells and the
CC   oligonucleotide; and determining the relative amount of Th1-biased
CC   cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC   specific claimed examples of such immunomodulatory oligonucleotides.
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

  Query Match            71.4%;  Score 15;  DB 20;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 19;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 12
```

```
AAV80103
ID   AAV80103 standard; DNA; 22 BP.
XX
AC   AAV80103;
XX
DT   12-MAR-1999  (first entry)
XX
DE   Immunomodulatory oligo comprising an ISS sequence.
XX
KW   Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW   ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW   human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW   B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    11
FT                    /*tag=  a
FT                    /note= "5-bromocytosine"
XX
PN   WO9855495-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998;   98WO-US11578.
XX
PR   06-JUN-1997;   97US-0048793.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Dina D,  Roman M,  Schwartz D;
XX
DR   WPI; 1999-059898/05.
XX
PT   Immunostimulatory oligonucleotides regulate the immune system - and
PT   contain an immune-stimulating octanucleotide sequence; for treating
PT   cancer, allergic and infectious diseases
XX
PS   Claim 24; Page 30; 63pp; English.
XX
CC   The invention relates to immunomodulatory oligonucleotides that comprise
CC   at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC   sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC   GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC   patients needing immune regulation, such as those suffering from cancer,
CC   an allergic disease and asthma. They are also used to prevent infectious
CC   diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC   and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC   Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC   Schistosoma. The immunomodulatory sequences are used to screen for human
CC   immunostimulatory activity by incubating macrophage cells and the
CC   oligonucleotide; and determining the relative amount of Th1-biased
CC   cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC   specific claimed examples of such immunomodulatory oligonucleotides.
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

  Query Match             71.4%;  Score 15;  DB 20;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 13
AAC64051
ID   AAC64051 standard; DNA; 22 BP.
XX
AC   AAC64051;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.
XX
KW   CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
KW   enhanced antigen presentation; antigen-presenting cell; APC;
KW   T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
KW   vaccine; ss.
XX
OS   Synthetic.
XX
PN   WO200062787-A1.
XX
PD   26-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US09664.
XX
PR   15-APR-1999;   99US-0292278.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Raz E,  Martin-Orozco E;
XX
DR   WPI; 2000-679548/66.
XX
PT   Enhancing antigen-presentation capabilities of T-cells for cancer
PT   immunotherapy, by contacting cells with an immunostimulatory
PT   oligonucleotide  -
XX
PS   Example I; Page 18; 42pp; English.
XX
CC   The invention relates to a method of inducing activation of T-cells
CC   to respond to an antigen, comprising contacting antigen-presenting cells
CC   (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
CC   thus treated have enhanced antigen presenting capabilities compared to
CC   antigen-activated APCs. APCs with enhanced antigen-presentation
CC   capabilities then present the antigen to T-cells. The method is useful
CC   for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
CC   antigen presenting capacity of tumour cells, thereby inducing T-cell
CC   activation, and is therefore useful for treating tumours. Additionally,
CC   tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.
CC   ISS-ODN treated APCs are induced to take up antigen through upregulation
CC   of Fc-receptor expression, to present antigen through upregulation of
CC   major histocompatibility complex (MHC) Class I and II expression and
CC   CD1d expression, to produce co-stimulatory factors (B7 and CD40), to
CC   provide cell-to-cell adhesion through upregulation of intercellular
CC   adhesion molecule (ICAM) expression, and to increase Th1 stimulatory
CC   cytokine production, all at levels greater than that achieved through
CC   contact of APC with antigen alone. The present sequence represents
CC   a phosphorothioate CpG ISS-ODN used in the exemplifications of the
CC   invention.
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

  Query Match             71.4%;  Score 15;  DB 21;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GAACGTTCGAGATGA 20
              |||||||||||||||
Db          8 GAACGTTCGAGATGA 22


RESULT 14
AAA96253
ID   AAA96253 standard; DNA; 22 BP.
XX
AC   AAA96253;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Sequence of a stabilised oligonucleotide with antitumour activity.
XX
```

KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
KW glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.
XX
OS Synthetic.
XX
PN WO200056342-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-FR00676.
XX
PR 19-MAR-1999; 99FR-0003433.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
XX
PI Carpentier A;
XX
DR WPI; 2000-602192/57.
XX
PT Use of stabilized oligonucleotides as antitumor agents, particularly
PT against nervous system tumors, have optimal activity and are not toxic
PT -
XX
PS Example 2; Page 16; 57pp; French.
XX
CC The present sequence represents a stabilised oligonucleotide which has
CC antitumour activity. The oligonucleotide comprises an octomer motif
CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where
CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
CC immunostimulatory, and are not toxic. They may be adapted for use in
CC animals or humans. The stabilised oligonucleotides are used for
CC treating tumours, of any type and any degree of anaplasia, particularly
CC human tumours in the peripheral or central nervous systems, specifically
CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTCGAGATGA 20
||||||||||||||||
Db 8 GAACGTTCGAGATGA 22

RESULT 15
AAA90458
ID AAA90458 standard; DNA; 22 BP.
XX
AC AAA90458;
XX
DT 10-JAN-2001 (first entry)
XX
DE CpG adjuvant oligonucleotide, SEQ ID NO:19.
XX
KW CpG oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;
KW microemulsion; adsorbent microparticle; vaccine; Th1 immune response;
KW viral infection; bacterial infection; parasitic infection; HCV; HBV;
KW hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;
KW human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;
KW rabies virus; cholera; diphtheria; tetanus; pertussis;
KW Helicobacter pylori; Haemophilus influenzae; malaria; ss.
XX
OS Synthetic.
XX
PN WO200050006-A2.
XX
PD 31-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-US03331.
XX
PR 26-FEB-1999; 99US-0121858.
PR 29-JUL-1999; 99US-0146391.
PR 28-OCT-1999; 99US-0161997.
XX
PA (CHIR) CHIRON CORP.
XX
PI O'Hagan D, Ott GS, Donnelly J, Kazzaz J, Ugozzoli M, Singh M;
PI Barackman J;
XX
DR WPI; 2000-587123/55.
XX
PT Microemulsion having an adsorbent surface comprising a microdroplet
PT emulsion consisting of a metabolizable oil and an emulsifying agent
PT which is a detergent, useful as a vaccine to treat bacterial, viral,
PT and parasitic infection -
XX
PS Claim 17; Page 40; 95pp; English.
XX
CC The invention relates to a microdroplet emulsion (microemulsion) with an
CC adsorbent surface, and which comprises a metabolisable oil and an
CC emulsifying agent (a detergent). It also relates to a composition
CC comprising the microemulsion and a microparticle with an adsorbent
CC surface, where the microparticle comprises a polymer selected from a
CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a
CC polycaprolactone, a polyorthoester, a polyanhydride, and a
CC polycyanoacrylate, and a second detergent. The surface of the
CC microparticles efficiently adsorb biologically active macromolecules such
CC as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes,
CC mediators of transcription or translation, metabolic intermediates and
CC adjuvants. Additionally, a second biologically active molecule may be
CC encapsulated within the microparticle. The microemulsion can be used in
CC methods of immunising a host animal, particularly a human, against a
CC viral, bacterial or parasitic infection, and in methods of increasing a
CC Th1 immune response. The microemulsions (having the appropriate antigens
CC adsorbed) may be particularly used as vaccines for hepatitis C virus
CC (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human
CC immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and
CC rabies virus; the bacteria which cause cholera, diphtheria, tetanus and
CC pertussis; Helicobacter pylori and Haemophilus influenzae; and
CC malaria-causing parasites. Sequences AAA90447-A90467 represent Th1
CC lymphocyte stimulating oligonucleotides containing at least one CpG motif
CC which are claimed for use as adjuvants in the compositions of the
CC invention.
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTCGAGATGA 20
||||||||||||||||
Db 8 GAACGTTCGAGATGA 22

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